

=> d his full

(FILE 'HOME' ENTERED AT 09:16:58 ON 30 DEC 2005)

FILE 'BIOSIS, MEDLINE, CAPLUS' ENTERED AT 09:17:45 ON 30 DEC 2005  
L1 1 SEA ALUSTXA OR ALUSTXY  
D L1 AB BIB  
L2 331 SEA DETERMIN? AND GENDER AND LOCUS  
L3 0 SEA L2 AND (SEX 5A TYPING)

FILE HOME

FILE BIOSIS  
FILE COVERS 1969 TO DATE.  
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT  
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 28 December 2005 (20051228/ED)

FILE MEDLINE

FILE LAST UPDATED: 29 DEC 2005 (20051229/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 will soon be available. For details  
on the 2005 reload, enter HELP RLOAD at an arrow prompt (=>).  
See also:

<http://www.nlm.nih.gov/mesh/>  
[http://www.nlm.nih.gov/pubs/techbull/nd04/nd04\\_mesh.html](http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html)  
[http://www.nlm.nih.gov/pubs/techbull/nd05/nd05\\_med\\_data\\_changes.html](http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html)  
[http://www.nlm.nih.gov/pubs/techbull/nd05/nd05\\_2006\\_MeSH.html](http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html)

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the  
MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate

FILE CAPLUS

Copyright of the articles to which records in this database refer is  
held by the publishers listed in the PUBLISHER (PB) field (available  
for records published or updated in Chemical Abstracts after December  
26, 1996), unless otherwise indicated in the original publications.  
The CA Lexicon is the copyrighted intellectual property of the  
American Chemical Society and is provided to assist you in searching  
databases on STN. Any dissemination, distribution, copying, or storing  
of this information, without the prior written consent of CAS, is  
strictly prohibited.

FILE COVERS 1907 - 30 Dec 2005 VOL 144 ISS 2  
FILE LAST UPDATED: 29 Dec 2005 (20051229/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply.  
They are available for your review at:

<http://www.cas.org/infopolicy.html>



NCBI Map Viewer

Alu STX<sub>9</sub>

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

Search

Find

Find in This View

Advanced Search

Homo sapiens Build 35.1

BLAST The Human Genome

Chromosome: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) [20](#) [21](#) [22](#) [ [X](#) ] [Y](#) [M](#)

Master Map: [Genes On Sequence](#) [Summary of Maps](#)

[Maps & Options](#)

Region Displayed: 89,376,720-89,377,580 bp

[Download/View Sequence/Entrez](#)

[Map Viewer Home](#)

[Map Viewer Help](#)

[Human Maps Help](#)

[FTP](#)

[Data As Table View](#)

[Maps & Options](#)

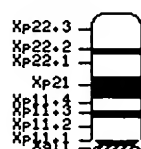
Compress Map ☐

Region Shown:

☐ out  
☐ zoom  
☐ in

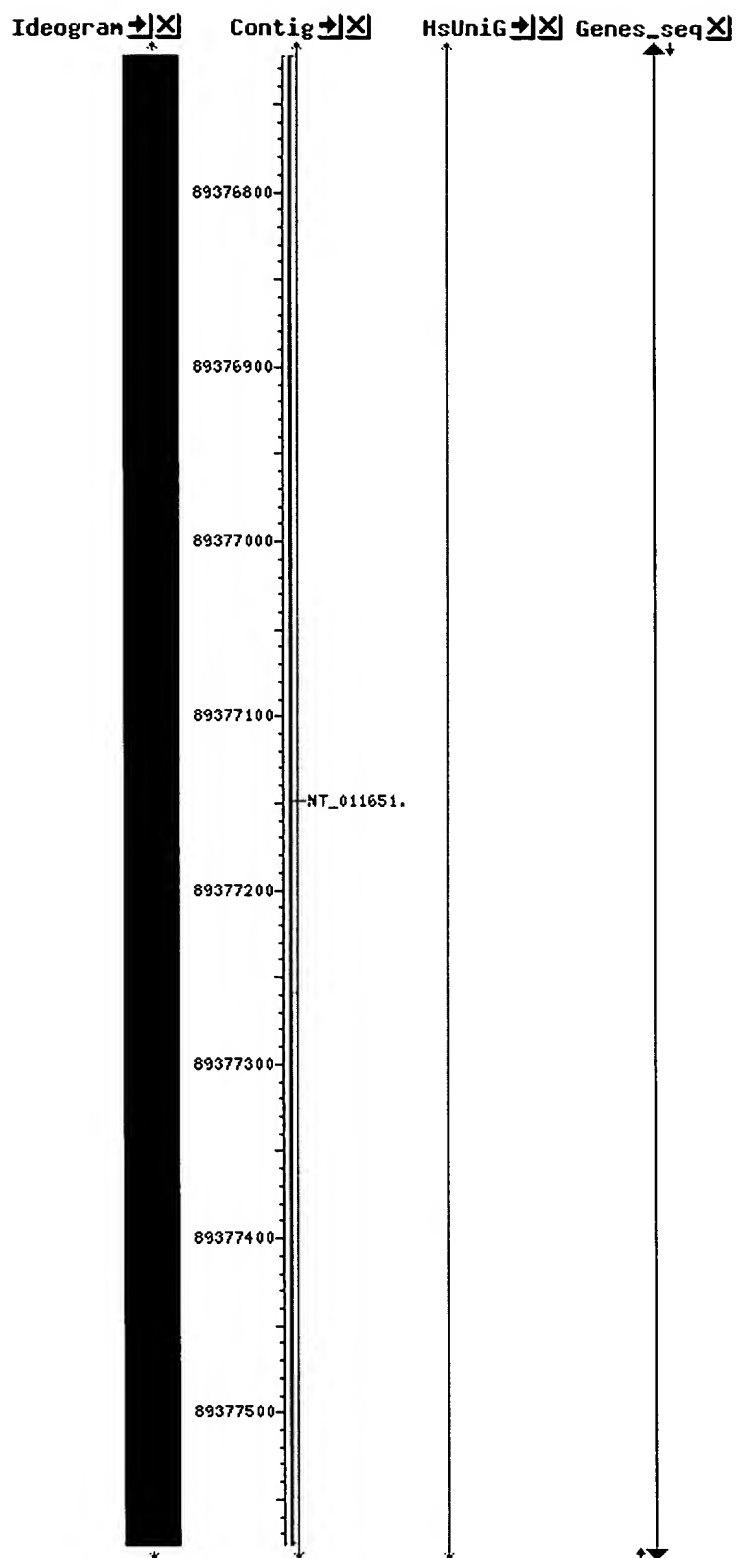
You are here:

**Ideogram**





- ☒ default
- ☐ master



**Summary of Maps:**

Map 1: Ideogram

Region Displayed: **Xq21.31**

Map 2: Contig

[Table View](#)

Region Displayed: **89,376,720-89,377,580 bp** [Download/View Sequence/Evidence](#)

Total Contigs On Chromosome: **26** [[5 not localized](#)]

Contigs Labeled: **1** Total Contigs in Region: **1**

Map 3: Human UniGene Clusters

[Table View](#)

Region Displayed: **89,376,720-89,377,580 bp** [Download/View Sequence/Evidence](#)

Total EST/mRNA alignments On Chromosome: **132438** [[673 not localized](#)]

UniGene Clusters Labeled: **0** Total EST/mRNA alignments in Region: **0**

Histogram Data: Tick Width=**1bp/pixel**, Max Height=**0 transcripts** (logarithmic scale)

Map 4: Genes On Sequence

[Table View](#)

Region Displayed: **89,376,720-89,377,580 bp** [Download/View Sequence/Evidence](#)

Total Genes On Chromosome: **1141** [[16 not localized](#)]

Genes Labeled: **0** Total Genes in Region: **0**

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)



NCBI Map Viewer

AluSTYq

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

Search

Find

Find in This View

Advanced Search

Map Viewer Home

***Homo sapiens* Build 35.1**

**BLAST The Human Genome**

Map Viewer Help

Human Maps Help

FTP

Data As Table View

**Maps & Options**

Compress Map ☐

Region Shown:

5,987,242

5,987,747

Go

Chromosome: [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [7](#) [8](#) [9](#) [10](#) [11](#) [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) [20](#) [21](#) [22](#) [X](#) [Y](#) [Mitochondrial](#)

Master Map: [Genes On Sequence](#) [Summary of Maps](#)

**Maps & Options**

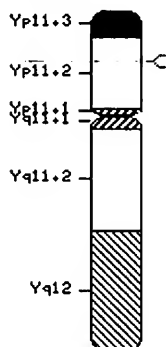
Region Displayed: 5,987,242-5,987,747 bp

[Download/View Sequence/Entrez](#)

out  
zoom  
in

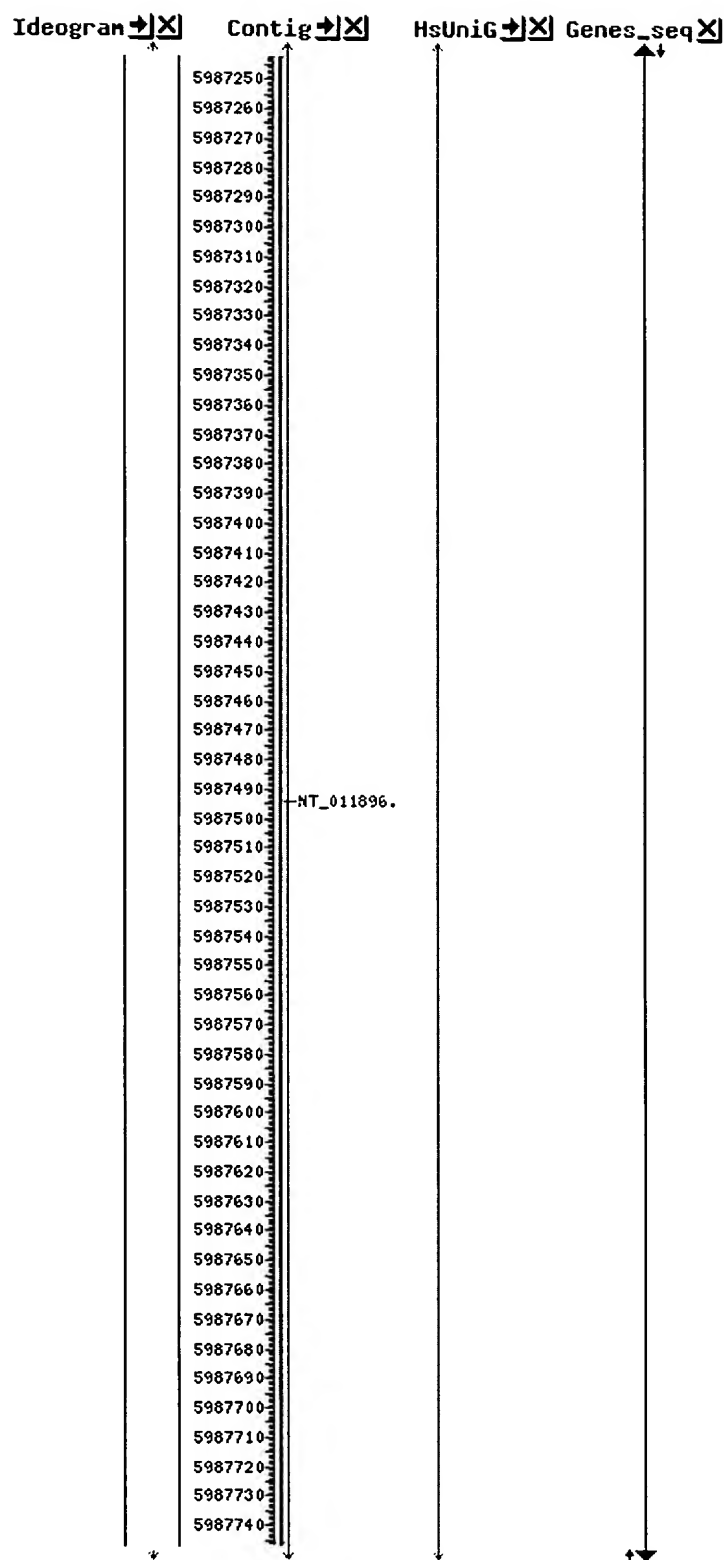
You are here:

**Ideogram**



☒ default

☐ master



### Summary of Maps:

Map 1: Ideogram

Region Displayed: Yp11.2

Map 2: Contig

Region Displayed: 5,987,242-5,987,747 bp

Total Contigs On Chromosome: 17

[Table View](#)

[Download/View Sequence/Evidence](#)

Contigs Labeled: 1 Total Contigs in Region: 1

Map 3: Human UniGene Clusters

[Table View](#)

Region Displayed: **5,987,242-5,987,747 bp** [Download/View Sequence/Evidence](#)

Total EST/mRNA alignments On Chromosome: **8310**

UniGene Clusters Labeled: **0** Total EST/mRNA alignments in Region: **0**

Histogram Data: Tick Width=**1bp/pixel**, Max Height=**0 transcripts** (logarithmic scale)

Map 4: Genes On Sequence

[Table View](#)

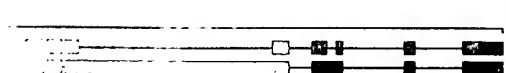
Region Displayed: **5,987,242-5,987,747 bp** [Download/View Sequence/Evidence](#)

Total Genes On Chromosome: **255**

Genes Labeled: **0** Total Genes in Region: **0**

[Disclaimer](#) | [Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)



All Databases

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Search  for    ☒ current

Limits

Preview/Index

History

Clipboard

Details

Display

Show

Send to

All: 1

Genes Genomes: 1

SNP GeneView: 1



☐ 1: **ZFX** zinc finger protein, X-linked [*Homo sapiens*]

GeneID: 7543 Primary source: [HGNC:12869](#)

updated 21

## Summary

**Official Symbol:** ZFX and **Name:** zinc finger protein, X-linked provided by HUGO Nomenclature Committee

**See related:** [HPRD:02445](#), [MIM:314980](#)

**Gene type:** protein coding

**Gene name:** ZFX

**Gene description:** zinc finger protein, X-linked

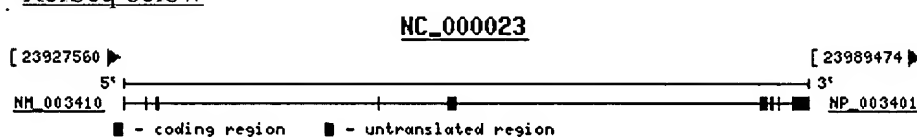
**RefSeq status:** Validated

**Organism:** *Homo sapiens*

**Lineage:** *Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo*

## Genomic regions, transcripts, and products

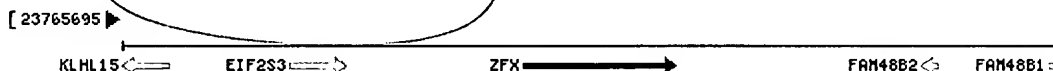
[RefSeq below](#)



## Genomic context

[See ZFX in MapViewer](#)

chromosome: X; Location: Xp21.3



## Bibliography

Gene References into Function (GeneRIF): [Submit](#)

[PubMed links](#)

## General gene information

### Markers

**G10526(e-PCR)** (Links: [UniSTS:38072](#))

Alternate names: CHLC.UTR\_01300\_X59739; CHLC.UTR\_01300\_X59739.P3

**ZFX(e-PCR)** (Links: [UniSTS:99002](#))

## Entrez Gene

Home  
About  
FAQ  
Help  
Search Toolbar  
Gene Handbook  
Statistics  
Downloads (FTP)

## Mailing Lists

Gene  
RefSeq

## Feedback

Help Desk  
Corrections  
About GeneRIFs

## Related Sites

BLAST  
Entrez Genome  
Genome Projects  
Genomic Biology  
GEO  
HomoloGene  
Map Viewer  
OMIM  
Probe  
RefSeq  
UniGene  
UniSTS

## Entrez

Global Search  
About | Help

## NCBI

Home  
Site Map  
Search



Alternate name: sWXD1468  
**G42693**(e-PCR) (Links: [UniSTS:140880](#))  
Alternate name: sY753  
**GDB:216882**(e-PCR) (Links: [UniSTS:156221](#))  
**Fabian\_Werner\_1**(e-PCR) (Links: [UniSTS:261928](#))  
**ZFX\_2118**(e-PCR) (Links: [UniSTS:281083](#))

### GeneOntology

Provided by [GOA](#)

#### Function

[DNA binding](#)

[DNA binding](#)

[metal ion binding](#)

[transcription coactivator activity](#)

[transcription regulator activity](#)

[zinc ion binding](#)

#### Process

[regulation of transcription](#)

[regulation of transcription, DNA-dependent](#)

#### Component

[nucleus](#)

#### Evidence

IEA

TAS [PubMed](#)

IEA

TAS [PubMed](#)

IEA

IEA

IEA

IEA

IEA

### Homology:

Mouse, Rat

[Map Viewer](#)

---

### General protein information

**Names:** zinc finger protein, X-linked  
zinc finger protein ZFX; X-linked zinc finger protein

---

### NCBI Reference Sequences (RefSeq)

**mRNA Sequence** [NM\\_003410](#)

**Source Sequence** [AC002404](#), [AF454950](#), [M30608](#)

**Product** [NP\\_003401](#) zinc finger protein, X-linked

**Consensus CDS (CCDS)** [CCDS14211.1](#)

**Conserved Domains (2)** [summary](#)

[COG5048](#): [COG5048](#); [FOG](#): Zn-finger [General function prediction only]

Location: 534 - 667 Blast Score: 98

[pfam04704](#): [Zfx\\_Zfy\\_act](#); [Zfx / Zfy transcription activation reg](#)

Location: 78 - 410 Blast Score: 1189

---

### Related Sequences

#### Nucleotide

**Genomic** [AF045780](#)

**Genomic** [AF045781](#)

**Genomic** [AF454948](#)

**Genomic** [AF454949](#)

**Genomic** [AY012072](#)

#### Protein

[AAL62492](#)

[AAC03062](#)

[AAL51082](#)

[AAL51083](#)

[AAG38815](#)

|      |                          |                          |
|------|--------------------------|--------------------------|
| mRNA | <a href="#">AB209892</a> | <a href="#">BAD93129</a> |
| mRNA | <a href="#">AF454950</a> | <a href="#">AAL51084</a> |
| mRNA | <a href="#">AF505615</a> | <a href="#">AAM33383</a> |
| mRNA | <a href="#">AF505616</a> | <a href="#">AAM33384</a> |
| mRNA | <a href="#">AF505617</a> | <a href="#">AAM33385</a> |
| mRNA | <a href="#">AF505618</a> | <a href="#">AAM33386</a> |
| mRNA | <a href="#">AF505619</a> | <a href="#">AAM33387</a> |
| mRNA | <a href="#">AY072770</a> | <a href="#">AAL67136</a> |
| mRNA | <a href="#">M30608</a>   | <a href="#">AAA61309</a> |
| mRNA | <a href="#">X59738</a>   | <a href="#">CAA42416</a> |
| mRNA | <a href="#">X59739</a>   | <a href="#">CAA42417</a> |
| mRNA | <a href="#">X59740</a>   | <a href="#">CAA42418</a> |
|      | None                     | <a href="#">P17010</a>   |
|      |                          | <a href="#">Q59EB9</a>   |
|      |                          | <a href="#">Q8NHZ1</a>   |
|      |                          | <a href="#">Q8NHZ2</a>   |
|      |                          | <a href="#">Q8NHZ3</a>   |
|      |                          | <a href="#">Q8NHZ4</a>   |
|      |                          | <a href="#">Q8NHZ5</a>   |
|      |                          | <a href="#">Q8WWU0</a>   |
|      |                          | <a href="#">Q8WXB7</a>   |
|      |                          | <a href="#">Q8WXB8</a>   |
|      |                          | <a href="#">Q8WXB9</a>   |
|      |                          | <a href="#">Q9BYX9</a>   |

---

### Additional Links

UniGene [Hs.370424](#)

MIM [314980](#)

HPRD [02445](#)

Display  Show  Send to

[Restrictions on Use](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLN](#) | [NIH](#)

SEQ ID 1

Get selected sequences

Select all

Deselect all

> ☐ gi|51511753|ref|NC\_000024.7|NC\_000024 ☒ Homo sapiens chromosome (Y) complete sequ  
Length=57701691

Score = 46.1 bits (23), Expect = 2e-04  
Identities = 23/23 (100%), Gaps = 0/23 (0%)  
Strand=Plus/Plus

|       |         |                         |         |
|-------|---------|-------------------------|---------|
| Query | 1       | CATGTATTTGATGGGGATAGAGG | 23      |
|       |         |                         |         |
| Sbjct | 5987242 | CATGTATTTGATGGGGATAGAGG | 5987264 |

→  
5987242      Alu STX<sub>9</sub>

5987747  
←

# SEQ ID 2

> gi|51511753|ref|NC\_000024.7|NC\_000024 **D** Homo sapiens chromosome Y, complete sequence  
Length=57701691

Score = 46.1 bits (23), Expect = 2e-04  
Identities = 23/23 (100%), Gaps = 0/23 (0%)  
Strand=Plus/Minus

|       |         |                          |         |
|-------|---------|--------------------------|---------|
| Query | 1       | CCTTTTCATCCAACCTACCACTGA | 23      |
|       |         |                          |         |
| Sbjct | 5987769 | CCTTTTCATCCAACCTACCACTGA | 5987747 |

# SEQ ID 3

> gi|51511752|ref|NC\_000023.8|NC\_000023 **D** Homo sapiens chromosome (X), complete sequence  
Length=154824264

Score = 50.1 bits (25), Expect = 2e-05  
Identities = 25/25 (100%), Gaps = 0/25 (0%)  
Strand=Plus/Plus

|       |          |                           |          |
|-------|----------|---------------------------|----------|
| Query | 1        | TGAAGAAATTCAGTTCATAGCTTGT | 25       |
|       |          |                           |          |
| Sbjct | 89376722 | TGAAGAAATTCAGTTCATAGCTTGT | 89376746 |

→  
89376722

AluSTXa

89377577  
←

# SEQ ID 4

> ☒ gi|51511752|ref|NC\_000023.8|NC\_000023 ☒ Homo sapiens chromosome X, complete sequence  
Length=154824264

Score = 46.1 bits (23), Expect = 2e-04  
Identities = 23/23 (100%), Gaps = 0/23 (0%)  
Strand=Plus/Minus

|       |          |                         |          |
|-------|----------|-------------------------|----------|
| Query | 1        | CAGGAGATCCTGAGATTATGTGG | 23       |
|       |          |                         |          |
| Sbjct | 89377599 | CAGGAGATCCTGAGATTATGTGG | 89377577 |